



## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/733,691  
Source: O I P E (IFWO)  
Date Processed by STIC: 12/30/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT  
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03; TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



## Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/733,691
<b>ATTN-NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/733,691

DATE: 12/30/2003

TIME: 11:25:40

Input Set : A:\10733691.txt

Output Set: N:\CRF4\12302003\J733691.raw

2 <110> APPLICANT: NIKOLICH, MIKELJON  
 3 HOOVER, DAVID  
 5 <120> TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS INCLUDING ROUGH PHENOTYPE BRUCELLA  
 HOST STRAINS  
 6 AND COMPLEMENTATION DNA FRAGMENTS  
 8 <130> FILE REFERENCE: ARMY 176  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/733,691  
 12 <141> CURRENT FILING DATE: 2003-12-11  
 14 <150> PRIOR APPLICATION NUMBER: US 60/402,164  
 W--> 15 US 60/533,016 → list these  
 17 <151> PRIOR FILING DATE: 2002-12-12  
 W--> 18 2003-09-15 → together  
 20 <160> NUMBER OF SEQ ID NOS: 2

## ERRORED SEQUENCES

*Do not insert  
Delete alphabetical  
headings, the CLF software will insert them.*

Does Not Comply  
Corrected Diskette Nodder      <150> US 60/533,016  
 <151> 2003-09-15

E--> 23 <210> SEQ ID NO: SEQ ID NO: 1      the CLF software will insert them.  
 24 <211> LENGTH: LENGTH: 2693  
 E--> 25 <212> TYPE: TYPE: DNA  
 26 <213> ORGANISM: ORGANISM: Brucella melitensis  
 W--> 27 <220> FEATURE: FEATURE:  
 E--> 28 <400> SEQUENCE: SEQUENCE: 1  
 29 caccttatgt ttgggacatt ttaatttagga acgtttatgc 40  
 30 cttcggatgc cgtgggcgtg gcatccgcat gagggatggc 80  
 31 tttgcgttgc tgcgctttga agatgttgaa attgggttag 120  
 32 ggcgcataa tgggtgtta agcctaccag catatgagg 160  
 33 tcgaaatttt gaggggttat ttcttcgccc caccgaagcc 200  
 34 actggattgg atggatatac agacccgttga tacgtcccc 240  
 35 atgctgaaca gccccgggttc atctttgcag acggagcagc 280  
 36 cctccacate aatagccctgt ttgcagataa taacaagggt 320  
 37 gatggcgtgt tttgcacaaa cgtccaaatac gtagatggaa 360  
 38 acgatctcaa ttcatccatc gacggccgaa ctgggttcaa 400  
 39 ttttatcaac gtagatcgca taaacatcaa tacgatccgc 440  
 40 agtggtgccc gccggaaatat ggcaccaggaa aatcttaaca 480  
 41 ctgtttccca aggtatctt ttgaatgcaa attgtcagac 520  
 42 tctaattata ggcaacgcag ttacccacaa ctgggtgaagt 560  
 43 cacggttttt atagccaagc tcaggacatt ttgggttaatg 600  
 44 gtctgatatac acgtgataat ggcggaaaggg ggtacgttgc 640  
 45 agagggttca gcagggtcat ctctccaaaa tggggccgtt 680  
 46 ttcaagatata atgttagcagg gaatttattt acaggaggga 720  
 47 caagcgtaaa ccatctcgcg aacttccaaac ttccataactc 760  
 48 tagcaccggg gggaaaactt ttgtggccaa tgtcaccaca 800  
 49 aatgggtctg cataacggtc cttgccattt taactataaa 840



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Input Set : A:\10733691.txt  
 Output Set: N:\CRF4\12302003\J733691.raw

50	ttagctattc	ccgcgcatta	agagtagaca	cggaaatca	880
51	gtatggctcc	gagacatatt	acagttatcc	taccagctaa	920
52	gtacccaggc	ggaagtcttc	gagttacgaa	aatatcggt	960
53	cgaatgcttt	tgaagggaag	tcagaattat	ggtgaacagt	1000
54	gtcaagttag	attggcagta	cgtgccata	cctacgatat	1040
55	tggggaggag	tttgcgtatc	ttatcgataa	tggtgttagag	1080
56	gttcggaaaa	tatcattcaa	agaagttcct	ccagaagatg	1120
57	ttaacaatgc	taactatttc	caaggtagaa	atatcgacct	1160
58	acagtcgaga	acctattggc	taatggagga	tggccaaaac	1200
59	aactgtcccg	atagtgcct	ttggctagtt	gtatcctact	1240
60	ctgttagagta	tcctattgcc	ccgataaggc	cgacactgtat	1280
61	atttgcacc	gatttcattc	aaaggtagct	acctgatatt	1320
62	atttggccac	cacggccccg	tgagggggat	gctgaggctc	1360
63	ttgcgttctt	acgacaatca	gacggcgta	tagctacaac	1400
64	accacacacg	cygctggatg	cgatttcata	cgctggctta	1440
65	cctgcgtcca	aagtttatct	tgctccgatg	gagtttgacc	1480
66	cgacgttttt	ggatcgttac	cggtcagtgt	ctaaggtaa	1520
67	ggaaccctat	ttcctttggc	caaccaaccc	aatgctcac	1560
68	aaaaaacatg	caaaagcggt	tcaagcgcta	gacctatatt	1600
69	acggcaaact	aaagggtaa	ataaaagacaa	agatagtcgg	1640
70	tgtgagtagt	gtgcggatgg	acccatccca	tcgatggcag	1680
71	gccaagtacg	aaaataaggc	ttatgtgaaa	tctgtacggg	1720
72	aaattgttgc	gggtctcgac	aacctgaaaa	gcaatgttga	1760
73	gttcgctgg	gaggttgcgg	acaaggagta	tgcggagctt	1800
74	cttgcattcag	tttgtttcct	ttggcatcca	actttggcag	1840
75	acaacggAAC	ttttgctgcg	gtcgaagcg	catatatggg	1880
76	atgtccaaacg	ctttcaaaacg	actacccgca	gatgcggtat	1920
77	atttctaacc	gtttcgaaat	tcccatgcag	tatTTtaacg	1960
78	caagtcgtgt	gaaggaaatg	gcatcagcgc	ttaagcaa	2000
79	ggaggagacg	ccaatagatg	taggttatt	gccaaagtgcga	2040
80	gaaaccctat	ctctgcattc	gtggaaagct	cacgcttccg	2080
81	aatactggga	tgtgatcg	agggcagcg	catgaaataag	2120
82	ctcggcgtgt	ttatcggtca	taacccagc	caatttagatc	2160
83	catatcaggg	tatttctcg	ttaatgc	tcgtgatcaa	2200
84	ggggccttg	aaccagggt	gcgggtaa	aattgttgc	2240
85	cccgctggc	taaaggacg	tgtacgttt	tttttggaa	2280
86	atgtgtat	cccacttgg	gcggtaaaa	ttatcgcgac	2320
87	gaatggtcag	cctccattgg	tttcgttatg	gaagttgaga	2360
88	gataagtcc	gtaagagacg	gacgagtaaa	cgaaaacgtc	2400
89	tctggctgg	gcgttatggs	aaaaatgtt	caaattttgt	2440
90	tgcagaatgg	ctttctttgc	gtcgtattt	ggggattttt	2480
91	ttggggctg	ctgcaattgc	tgtatgtact	attctacttg	2520
92	ccgtaccaat	tgtatagcc	ttcacccgctc	ttatcggtct	2560
93	tctatttgct	cgtcgctta	ttagacgtgt	tatcaggta	2600
94	aagcttgg	tgtttttca	aaaaatgcc	aatcaattca	2640
95	acaattaaat	gtcatctgt	gaaaccatcg	accggatgag	2680
96	ggaacggaa	tcc	2693		

OK  
 E--> 98 <210> SEQ ID NO: SEQ ID NO 2  
 99 <211> LENGTH: LENGTH 410

*delete*

## BEST AVAILABLE COPY

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/733,691

DATE: 12/30/2003  
TIME: 11:25:40

Input Set : A:\10733691.txt  
Output Set: N:\CRF4\12302003\J733691.raw

E--> 100 <212> TYPE: **TYPE: PRT**  
 101 <213> ORGANISM: **ORGANISM: Brucella melitensis**  
 E--> 102 <400> SEQUENCE: **SEQUENCE: 2**  
 103 Met Ala Pro Arg His Ile Thr Val Ile Leu  
 E--> 104        105                          10  
 105 Pro Ala Lys Tyr Arg Gly Gly Ser Leu Arg  
 E--> 106        105                          20 20  
 107 Val Thr Lys Asn Ile Val Arg Met Leu Leu  
 E--> 108        25                          30  
 109 Lys Gly Ser Gln Asn Tyr Gly Glu Gln Cys  
 E--> 110        35                          40  
 111 Gln Val Arg Leu Ala Val Arg Ala Asp Thr  
 E--> 112        45                          50  
 113 Tyr Asp Ile Gly Glu Glu Phe Arg Asp Leu  
 E--> 114        55                          60  
 116 Ile Asp Asn Gly Val Glu Val Arg Glu Ile  
 E--> 117        65                          70  
 118 Ser Phe Lys Glu Val Pro Pro Glu Asp Val  
 E--> 119        75                          80  
 120 Asn Asn Ala Asn Tyr Phe Gln Gly Arg Asn  
 E--> 121        85                          90  
 122 Ile Asp Leu Gln Ser Arg Thr Tyr Trp Leu  
 E--> 123        95                          100  
 124 Met Glu Asp Gly Gln Asn Asn Cys Ala Asp  
 E--> 125        105                          110  
 126 Ser Asp Leu Trp Leu Val Val Ser Tyr Ser  
 E--> 127        115                          120  
 128 Val Glu Tyr Pro Ile Ala Pro Phe Arg Pro  
 E--> 129        125                          130  
 130 Thr Leu Ile Phe Ala Thr Asp Phe Ile Gln  
 E--> 131        135                          140  
 132 Arg Tyr Val Pro Asp Ile Ile Trp Pro Pro  
 E--> 133        145                          150  
 134 Arg Pro Gly Glu Gly Asp Ala Glu Ala Leu  
 E--> 135        155                          160  
 136 Ala Phe Leu Arg Gln Ser Asp Gly Val Leu  
 E--> 137        165                          170  
 138 Ala Thr Thr Pro His Thr Arg Leu Asp Ala  
 E--> 139        175                          180  
 140 Ile Ser Tyr Ala Gly Leu Pro Ala Ser Lys  
 E--> 141        185                          190  
 142 Val Tyr Leu Ala Pro Met Glu Phe Asp Pro  
 E--> 143        195                          200  
 144 Thr Phe Leu Asp Arg Tyr Arg Ser Val Ser  
 E--> 145        205                          210  
 146 Lys Val Lys Glu Pro Tyr Phe Leu Trp Pro  
 E--> 147        215                          220  
 148 Thr Asn Pro Asn Ala His Lys Asn His Ala  
 E--> 149        225                          230

*misaligned  
amino acid numbers  
( see item 3 on Error  
summary sheet )*

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Input Set : A:\10733691.txt  
Output Set: N:\CRF4\12302003\J733691.raw

150 Lys Ala Phe Gln Ala Leu Asp Leu Tyr Tyr  
E--> 151 235 240  
152 Gly Lys Leu Lys Gly Lys Ile Lys Thr Lys  
E--> 153 245 250  
154 Ile Val Gly Val Ser Ser Val Arg Met Asp  
E--> 155 255 260  
156 Pro Ser His Arg Trp Gln Ala Lys Tyr Glu  
E--> 157 265 270  
158 Asn Lys Ala Tyr Val Lys Ser Val Arg Glu  
E--> 159 275 280  
160 Ile Val Ala Gly Leu Asp Asn Leu Lys Ser  
E--> 161 285 290  
162 Asn Val Glu Phe Ala Gly Glu Val Ala Asp  
E--> 163 295 300  
164 Lys Glu Tyr Ala Glu Leu Leu Ala Ser Ala  
E--> 165 305 310  
166 Cys Phe Leu Trp His Pro Thr Leu Ala Asp  
E--> 167 315 320  
168 Asn Gly Thr Phe Ala Ala Val Glu Ala Ala  
E--> 169 325 330  
170 Tyr Met Gly Cys Pro Thr Leu Ser Asn Asp  
E--> 171 335 340  
172 Tyr Pro Gln Met Arg Tyr Ile Ser Asn Arg  
E--> 173 345 350  
174 Phe Glu Ile Pro Met Gln Tyr Phe Asn Ala  
E--> 175 355 360  
176 Arg Ser Val Lys Glu Met Ala Ser Ala Leu  
E--> 177 365 370  
178 Lys Gln Met Glu Glu Thr Pro Ile Asp Val  
E--> 179 375 380  
180 Gly Leu Leu Pro Ser Arg glu Thr Leu Ser  
E--> 181 385 390  
182 Leu His Ser Trp Glu Ala His Ala Ser Glu  
E--> 183 395 400  
184 Tyr Trp Asp Val Ile Val Arg Ala Ala Ala  
E--> 185 405 410

*Same*

*end*

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/733,691

DATE: 12/30/2003  
TIME: 11:25:41

Input Set : A:\10733691.txt  
Output Set: N:\CRF4\12302003\J733691.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:  
L:18 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:  
L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:25 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:27 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:28 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:96 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:2693 SEQ:0  
L:98 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:100 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:102 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:104 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0  
M:332 Repeated in SeqNo=0  
L:185 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:410 SEQ:0